124494 Human antig COG65617 Sequence CO921958 Sequence BV209629 TNFRSF7_2 GO6406 human STS W AKO5500 Homo sapi CO070114 Sequence CO136705 Sequence CO136705 Sequence CO136705 Sequence CO226428 Sequence CO226428 Sequence CO236428 Sequence CO236428 Sequence CO236428 Sequence CO2107931 Sequence CO110704 Sequence CO110704 Sequence CO2108470 Sequence CO2108470 Sequence CO211024 Sequence CO211029 Sequence CO211039 Sequence

OM nucleic

Run on:

Seguence:

Searched:

Database

Result No.

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BUU15201
TLISB Cell Burface antigen and CD27 Cell Burface antigen, and
Utilization thereof.
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04-0CT-2000 US
553759
BRIAN SEED, ALEJANDRO ARUFFO, MARTIN AMIOT
C12N15/09, CO71X4/725, G01N33/53, C12N15/00
TLiSa cell surface antigen and CD27 cell surface antigen, and utilization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae; Homo.

1 (bases I to 1201)
Seed, B., Aruffo, A. and Amiot, M.
TLiSa cell surface antigen and CD27 cell surface antigen, and utilization thereof
Patent: JP 2001157592-A 19 12-JUN-2001;
THE GENERAL HOSPITAL CORP
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Pred. No. 1.6e-271;
0; Mismatches 4; Indels 1;
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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CQ271024
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JP 2001157592-A/19
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JP 2001157592-A/19.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 99.6%;
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BC012160 Homo sapi
CQ721666 Sequence
CQ869520 Sequence
CS119000 Sequence
CS119692 Sequence
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AX818155 Sequence
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                                                                                                              December 7, 2005, 00:51:17; Search time 6317 Seconds
                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                        5883141 segs, 28421725653 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                  - nucleic search, using sw model
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BC095844
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Maximum DB seq length: 2000000000
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Unclassified.

SE 1 (bases 1 to 1204)

AS Cocks.B.G., Stuart,S.G. and Seilhamer,J.J.

Compositions for the detection of blood cell and immunological response gene expression

The Patent: US 6607879-A 1227 19-AUG-2003;

Incyte Corporation; Palo Alto, CA

Incyte Corporation; Palo Alto, CA

Location/Qualifiers

Location/Qualifiers

//mol_type="genomic DNA"
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GCAGGAGCCCAGCCAGCTGCGCGCGCG-TGCAGGAGGGCGGGGGCTCTGGTTGTAAGGCA
                1081 GCAGGAGCCCAGCCAGCTGCGCTGCAGGAGGCGGGGGGGCGCTCTGGTTGTAAAAACA
                                                            CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC
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Pred. No. 1.6e-271;
0; Mismatches 4;
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                  CTGCACTACAGCCCTGGCCTCCACCCCCACCCGACCATCCAAGGGAGAGTGAGACC
                                                                                                                    CTGCACTACAGCCCTGGCCTCCACCCCCCCGCCGACCATCCAAGGGAGAGTGAGACC
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GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT
                                      CCAGGAGAATTACCGAAAACCGGAGCCTGCTGCTCCCCCTGAGCCAGCACCTGCGGTAG
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Patent: WO 03068268-A 26 21-AUG-2003;
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Bukaryota, Metazoa, Chordata; Craniata; Primates; Catarrhini;
Hominidae, Homo.
1 (bases I to 123)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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                                                                                                                                                                                                CGATITITATICGCATCCTIGIGATCTICTCTGGAATGTICCTIGITITCACCCTGGCCGG
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/product="T-cell activation antigen"
/product="T-cell activation antigen"
/protein_id="AAASBA11:"
/db_xref="G1:100085"
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QTLADPRQLPARTISTWPPQRSLCSSDF1RILV1FSGMMFLWFTLAGALFLHQRRKKYR
SNKGSSPVEPAEPCRYSCPREEEGST1P1QEDYRKPEPACSP"
           PRI 31-DEC-1994
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
Homo sapiens T cell activation antigen (CD27) mRNA, complete cds. M63928. GI:180084
T-cell activation antigen CD27. Homo sapiens (human)
Homo sapiens (human)
F-cell activation antigen CD27.
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                                                                                                                                                                                 Camerini, D., Walz, G., Loenen, W.A., Borst, J. and Seed, B.
The T cell activation antigen CD27 is a member of the nerve factor/tumor necrosis factor receptor gene family
J. Inmunol. 147 (9), 3165-3169 (1991)
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.larity 99.6%; Pred. No. 1.6e-271;
Conservative 0; Mismatches 4; Indels 1;
                                                                                                                                                                                                                                                                source text: Homo sapiens CDNA to mRNA Location/Qualifiers
                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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/db_xref="taxon:9606"
1. .1204
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/gene="CD27"
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/gene="CD27"
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QTLADFRQLPARTLSTHWPPQRSLCSSDFIRILVIFSGMFLVFTLAGALFLHQRRKYR
SNKGBSPVEPAEPCRYSCPREEEGSTIFIQEDYRKPEPACSP"
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                                                                                                                                  Score 1182.6; DB 8;
Pred. No. 1.6e-271;
0; Mismatches 4;
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Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramaon, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richard, S.W., Worley, K.C., Hale, J.A., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Marny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 29 Row: h Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Autobrogram, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, Milliam Chow, Alison Cloutier, Ruth Reatherstone, Malachi Griffith, Obl Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Bravaneh Saeedi, JR Sancos, Angelique Schnerch, Ursula Skalska, Buane Smallus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
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PGTFLVKDCDQHRKAAQCDPCIPGVSFSPDHHTRPHCESCRHCNSGLLVRNCTITANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/product="tumor necrosis factor receptor superfamily,
member 7, precursor"
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/db_xref="GeneID:939"
/db_xref="MIM:186711"
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Contact: MGC help deak
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis Staudt
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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/tissue type="Primary B-Cells from Tonsils"
/clone lib="NIH MGC 48"
/lab_host="DH10E-R"
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/db_xref="GI:15082491"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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1987.980
/gene="TNFRSF7"
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	DECTRECT GCACTTGCCCGGGACTCTCTCTCTCTCTCTCTCTCTCTTGTTTTCCCCTGTGCACTCCCCGAAGATCCCCTGTGCAGCTCCCTGTGCAGCTCCCTGTGCATCTCTTGTTTTTCACCTTGCTTTTTTTT	841 901 901 961 1021	1021 GAGTGCCTTTTCGAGACTGGCAGCACAAATATGGATGAGGAGGAGAAATATGGATGAAATATGGATGAGAAATATGGATGAGAAATATGGATGAGAAATATGGATGAGAGAGTGGGAAAATATGGATGAGGAG	RESULT 8 CQ869620 CQ869620 CQ869620 CQ869620 DEFINITION Sequence 41 from Patent WO2004074320. ACCESSION CQ869620 VERSION CQ869620.1 GI:51999481 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
0y 961 TGGCAGCCACAACTGCAGTCCCATCCTCTTCAGGGCCCTTTCCTGTACACGTGACA 1020 Db 1058 TGGCAGCCACAACTGCAGTCCTTTTCTCAGGCCCTTTCTTT	RESULT 7 CQ721686 LOCUS LOCUS LOCUS ACCESSION CQ721686.1 G1:42282543 VERSION CQ721686.1 G1:42282543 VERYNORDS SOURCE Momon sapiens Fundancial Homo sapiens Fundancial Euchontoglires; Primates; Euteleostomi; Hominidae; Homo. REFERENCE AUTHORS Venter C.J. Adams M.C. Li.P.W. and Myers.E.W.	Kits, such as nucleic acid arrays, compris humanexons or transcripts, for detecting expenses. WO 02068579-A 7620 06-SEP-2002; PE Corporation (NY) (US) Location/Qualifiers 1. 1204 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	Query Match 98.4%; Score 1181; DB 6; Length 1204; Best Local Similarity 99.5%; Pred. No. 3.8e-271; 1.6ab 5; Indels 1; Gaps 1; Matches 1195; Conservative 0; Mismatches 5; Indels 1; Gaps 1; 1. GGGGGCAAAGAAGAAGACAGCAGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCA 60 Qy 1 GGGGTGCAAAGAAGAAGAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAACACAGAGACAAGAAGAACAGAACAGAACAGAACAGAACAGGACCATGGCGACAAGACACACATGGGCAAGAACAGAAAGAA	OY 181 CCCAGAGAGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240

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Gene expression profiling of colon cancer by dna microarrays and correlation with survival and histoclinical parameters

Batent: WO 2005054508-A 1047 16-UNN-2005;

Ipsogen (FR); Institut Paoli-Calmettes, Ipc (FR); Institut National de la Sante et de la Recherche Medicale (INSERM) (FR)

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                                               938 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGGAG
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                                                                                 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCGGACCATCCAAGGGAGAGTGAGACC
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/note="tumor necrosis factor receptor superfamily,
7(TNFRSF7) gene."

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Mol type="unassigned DNA"
/db_xrefe="taxon 32630"
/noTe="Description of Artificial sequences:primer"
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0; Mismatches 5;
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CS119000.1 GI:70666946
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                                                                                                                                                                                                                                                                                                                                    GGGGTGCAAAGAAGAGACAGCAGCCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT
                                                                                                                                                                                                                                                                       Gaps
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                        ï
                                                                                                                                                                                                                                     Length 1300;
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                       Score 1181; DB 6;
Pred. No. 3.8e-271;
0; Mismatches 5;
                                                 Morris, D.W., Morris, D.W. and Malandro, M.S
                                                                 Novel therapeutic targets in cancer
Patent: WO 2004074320-A 41 02-SEP-2004;
Sagres Discovery, Inc. (US)
Location/Qualifiers

    .1300
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.5%;
Matches 1195; Conservative
               Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278
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Location/Qualifiers

1. 783

Arganism="synthetic construct"

Amol type="mRNN"

Ab xref="taxon:32630"

Aclone="FLH021597.01L"

Alab host="Escherichia coli DH5alpha Tl resistant"

Anote="derived from Homo sapiens first strand cDNA library
BD In-Fusion(TM) cloning system between the SalI and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Each clone is clonally isolated and full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Direcin id="AAX42818.1"

/db_xref="GI:61366131"

/db_xref="GI:6134"

/dr_cranslat_ion="MARPHPWMLCVLGTLVGLSATPAPKSCPERHYWAQGKLCCQMCE

PGTFLVKDCDCHRKAAQCDPCIPGVSFSPDHHTRPHCESCRHCNSGLLVRNCTITANA

ECACRNGWQCRDKECTECDPLNNPSLTARSSQALSHPQPFHILPYVSEMLEARTAGHM

QTLADFRQLPARTLSTHWPPQRSLCSSDFIRILVIFSGMFLVFTLAGALFLHQRRKYR

SNKGESPVEPAEPGRYSCPREBEGSTIPIQEDYQKPEPACSPL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 ACTCCAGCCCCCAAGAGCTGCCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 779.4; DB 11; Length 783;
Pred. No. 3.2e-175;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                           from placenta and brain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon start=1
trans1 table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1058 TGGCAGCCACAACTGCAGCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (05-7AN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA canbridge, MA 02141, USA a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned without srop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using
                                                                                                                           817
                                                                                                                                                                                        780
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Hines,L., Rolfs,A., Jepson,D., Moreira,D., Raphael,J., Kelley,F.,
Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E.,
Williamson,J. and LaBaer,J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hines L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and LaBaer, J.
698 GCAGCTGCCTGCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC
                                                          CGATITIATICGCAICCTIGIGATCTICICIGGAAIGITCCTIGITTTCACCCTGGCCGG
                                                                                                                                                                                                                                               GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGAGGCAGCACCATCCCCAT
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1 (bases 1 to 783)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Sciurcognathi; Burchontoglires; Murinas; Musinas;
1 (bases 1 to 1585)
2 (bases 1 to 1585)
3 (bases 1 to 1585)
4 (bases 1 to 1585)
6 (bases 1 to 1585)
6 (bases 1 to 1585)
7 (bases 1 to 1585)
8 (bases 1 to 1585)
9 (bases 1 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Original source text: Mus musculus (strain B6/CBAFIJ) (library:
oligo dT in lambda ZAP) female Juvenile, 6-8 weeks thymus CDNA to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 GAGAGTGAGACCTGGAGGCGACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGT
                                               GTACACGTGACAGAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGT
                                                                                                                                            GGAGAGTGGGAAGCAGGCCCAGCCAGCTGCGCGCGCG - TGCAGGAGGGCGGGGGCTCT
                                                                                                                                                                     421 GGAGAGTGGGAAGCAGGCCAGCCAGCTGCGCCTGCGCGCTGCAGAGGGCGGGGGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 GGGCACAGAAAGGAGCCGCCTGGGCAGGACCATGGCACGACACATCCCTGGTGGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 GCGTTCTGGGGACCCTGGTGGGCTCTCAGCTACTCCAGGCCCCCAAGAGCTGCCCAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 GGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAACATTCCTCG
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                                                                           361 GTACACGTGACAGAGTGCCTTTTCGAGACTGGCAGGACGACGACAAATATGGATGAGGT
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                                                                                                                                                                                                                                         1128 GGTTGTAAGGCACACTTCCTGCTGCGAAAGACCCCACATGCTACA 1171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="thymus"
/dev stage="Juvenile, 6-8 weeks"
/tissue_lib="oligo dT in lambda ZAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.6%; Score 451.8; DB 9; ilarity 73.2%; Pred. No. 5e-97; Conservative 0; Mismatches 202;
                                                                                                                                                                                                                                                                                                                                                                                                                 MUSCD27A 1585 bp mRNA mus musculus CD27 antigen (Cd27) mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Immunol. 23 (4), 943-950 (1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/strain="B6/CBAFIJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L24495.1 GI:403146
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                           CTTGTTTTCACCCTGGCCGGGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haferlach, T., Schoch, C., Kern, W., Kohlmann, A., Schnittger, S., Dugas, M., Eils, R., Brors, B. and Mergenthaler, S.
Novel genetic markers for leukemias
Patent: WO 03039443-A 422 15-WAY-2003;
Deutsches Krebsforschungszentrum (DE);
Ludwig-Maximilian-Universitaet Muenchen (DE); Haferlach, Torripp Dr. (DE); Schoch, Claudia (DE); Kern, Wolfgang (DE)
Location/Qualifiers
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Pred. No. 8.1e-110;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    524 bp DN Sequence 422 from Patent WO03039443.
AX778265

    .524
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Best Local Similarity 99.0
Matches 519; Conservative
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College of Wisconsin Copen Biosystems CDNA Library Preparation: Open Biosystems CDNA Library Arrayed by: The I.M.A.G. Consortium (LLNL) CDNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 227 Row: c Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /trānslation="MAWPPLYWLCMLGTLVGLLATPAPNNCPDRHYWIGAGLCCQMCG
PGTFLVKHCDDRAAAQCDPCIPGTSFSPDYHTRPHCESCRHCNSGFLIRNCTVTANA
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LPDSTVYSKLESQPSELSSDCIRIFYTFSSWLLVFVLGGILFFHQRRNHGPNEDSQAV
PERLCPYSCPREEEGSVIPIQEDYRKPEPASYP"
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Submitted (06-MAY-2005) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGCCACATCCCTGGTGGCTGT
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Tigsue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
                                                                                      human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/product="hypothetical protein LOC500318"
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/db_xref="GeneID:500318"
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clone_lib="NIH_MGC_251"
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/note="Vector: pExpress1"
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.E., Toshiyuti, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbe, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Schurognathi, Muroidea, Muridae, Murinae, Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAACTCGACTGTCTATAGCCAGCGGTCATCCCATAGACCCCTGTGCAGCTCGGACTGCA
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                         GICTICICGITCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCGCAATGGCT
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Rattus norvegicus
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Hominidae, Homo.

E. I (bases I to 17257).

S. Muzny, D.M., Adams, C., Addo-Oduola, B., Ali-osman, F.R., Allen, C., Alabrooke, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Babrooke, S.L., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Banedra, J., Benton, J., Bimed, Brown, B., Brown, M., C., Burch, P., Burket, C., Burrell, K.L., Byrd, N.C., Carron, T.R., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C. Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., Delaney, K.R., Delgado, O., Penn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S.,
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Homo sapiens 12 PAC RPS-940J5 (Roswell Park Cancer Institute Human
PAC Library) complete sequence.
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152 GACACTACTGGATTGGGGCAGGACTCTGCTGCCAGATGTGTGGGGCCAGGGACATTCCTTG 211
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                               GTTTTCTCATCCCCAACTGCACGCTCACTGCCAATGCTGAGTGCACCTGTTCCAAGGGCT
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ESCOTTO, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gaccia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Guevara, W., Gunaratne, P., Hale, S., Haris, Gorrell, J. H., Guevara, W., Gunaratne, P., Hart, M., Havlak, P., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holluns, B., Homai, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Corhikhes, I., Jackson, E., Karlsson, E., Kelly, S., Khan, U., Konyar, C., Kardovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lucier, R., Luna, R., Martinaz, E., Martinaz, E., Massey, E., Martinaz, R., Martinaz, E., Martinaz, R., Martinaz, E., Marshiney, E., McLeod, M.P., Meador, M., Mai, J., Mahashwari, M., Mapua, P., Martinaz, E., Moser, M., Miller, A., Miner, G., Marer, Z., Mitchell, T., Moreton, D., Newtson, J., Newtson, N., Nguyen, N., Notedo, R., Nokenkwo, S., Oguh, M., Okwnou, G., Oragunye, N., Ovidoo, R., Pace, A., Payton, B., Peery, J., Perez, L., Schers, R., Primus, E., Pu, L.L., Quiles, M., Rolls, S., Sodergren, E., Sonaike, T., Shan, H., Stanley, H., Stone, H., Sutten, A., Svatek, A., Tabor, P., Tamerisa, A., Tang, H., Tang, H., Tang, H., Tang, H., War, M., War, W., W., Washington, C., Watliams, G., Williams, G., Williamson, A., Roberlapati, R., Roles, M., Williams, G., Williams, G Direct Submission
Submitted (15-WAR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 172571) Submitted (01-FEB-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Feb 1, 2003 this sequence version replaced gi:4572650.

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu Submitted (07-APR-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Direct Submission Submitted (26-NOV-1998) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 172571) (bases 1 to 172571) (bases 1 to 172571) Direct Submission Unpublished Direct Submission Direct Submission Worley, K.C. Worley, K.C. Worley, K.C. Worley, K.C. TITLE JOURNAL REFERENCE AUTHORS REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL JOURNAL COMMENT

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Peatures listing.

ANNOTATION OF FEATURES: STSs are identified using ePCR (Genome Res. 7:541-550) searches STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST

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(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
                                                    EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
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SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:

http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht ml.

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complement (6084. .6101)
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## ALIGNMENTS

us-09-836-544c-28.rng

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This nucleotide sequence comprises human CD27 cDNA. The cDNA was isolated from a human T lymphocyte cDNA library using a novel method for cloning cDNAs from mammalian expression libraries. The method is based on transient expression of an antigen in eukaryotic cells and physical selection of cells expressing the antigen by adhesion to an antibody-coated substrate. The method is useful for the isolation and molecular cloning of any protein which can be expressed and transported to the cell surface membrane of a eukaryotic cell. It has been used to clone genes contage (see AAW63442-61) encoding cell surface antigens from mammalian lymphocytes (see AAW6340440-55). The purified genes and proteins are useful for immunodiagnostic and immunotherapeutic applications, including the diagnosis and treatment of immuno-mediated infections, diseases, and diagnosis and treatment of immuno-mediated infections, diseases, and flagnosis and animals, including humans. CD27 (see AAW80451), a T lymphocyte activation antigen, has been expressed in COS cells. (Updated on 25-MAR-2003 to correct PR field.)
New cloning vector and poly:linker - based on existing sequences for efficient cloning and expression of mammalian cDNA(s), especially human lymphocyte antigenic sequences.
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Seguence 1200 BP; 260 A; 373 C; 341 G; 226 T; 0 U; 0 Other;

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Aruffo A;

Simmons D,

Allen J,

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cDNA encoding human CD40 antigen - useful for cloning cDNA encoding cell surface antigens, constructing cDNA libraries, expressing vectors for expression in eukaryotic cells or their fragments.
                                                Example 13; Col 65-66; 79pp; English
Lauffer L,
          WPI; 1999-069813/06.
P-PSDB; AAW86198.
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Sequence 1200 BP; 260 A; 373 C; 341 G; 226 T; 0 U; 0 Other;

CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGACCATGGCACGGCCACATCCCTG 120 GIGGCIGIGCGIICIGGGGACCCIGGIGGGCTCICAGCIACICCAGCCCCCCAAGAGCIG 180 9 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT GOGGTGCAAAGAAGAGACAGCAGCCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT ö DB 2; Length 1200; 0; Indels Query Match 100.0%; Score 1200; Best Local Similarity 100.0%; Pred. No. 0; Matches 1200; Conservative 0; Mismatches 61 61 121 121 g ઠે 셤 ð 8 8 8

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BP AAS03189 standard; cDNA; 1200 AAS03189

RESULT

Human T-lymphocyte specific antigen CD27 cDNA sequence.

(first entry)

29-AUG-2001

Human; T-lymphocyte specific antigen; immune-mediated disease; CD27; infection; immune deficiency disorder; hypersensitivity; inflammation; systemic lupus erythematosus; platelet disorder; rheumatoid arthritis; transplant rejection; asthma; ss.

Homo sapiens

.202, aa:Arg) /product= "CD27 antigen" /trans1 except= (pos:200. 101. .160 Location/Qualifiers 101. .883 /*tag= b 161.880 /*tag= c /*tag= a sig_peptide mat_peptide Key 

92US-00983647 01-DEC-1992; 17-APR-2001

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encoding for human T-lymphocyte specific antigen CD27 is 1 of various human lymphocyte cell surface antigen cDNA sequences (AAS03112, AAS03113, AAS03115, AAS03115). Aescribed in the present invention. The invention relates to a novel method of cloning cDNA encoding cell surface antigens and efficient construction of cDNA encoding cells and described are 2 expression vectors (AAS03171, AAS03174) which provide high level expression vectors (AAS03171, AAS03174) which provide high level expression in eukaryotic host cells. A genetically engineered cDNA sequence encoding the CD28 amino acid extracellular domain sequence (amino acids 1-134 given in AAU02437) and/or comprising nucleotides 100-759, 154-555 or 154-759 of the CD28 cDNA sequence (AAS03175) is also new. The purified genes and proteins are useful for immunodiagnostic and immunotherapeutic applications, such as in the diagnosis and treatment of immune-mediated diseases, infections or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorders in animals and humans. Such diseases include immune deficiency diseases, diseases of immediate type of hypersensitivity, asthma, hypersensitivity pneumonitis, systemic lupus erythematosus, rheumatoid arthritis, acute and chronic inflammation, platelet disorders, plasma and other cell neophasms, parasitic diseases, multiple sclerosis, Guillain-Barre syndrome and tissue and organ transplant rejection. The sequence can also be used to identify, isolate and purify other antibodies and
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                                                                 89US-00160416.
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90US-00553759.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A cDNA clone encoding CD27 was obtained from human T lymphocyte cDNA transferred into COS cells and immunoselected using the MAbs OKT18a and CLB-9F4 (see e.g. AAQ21164 for description of the rapid immunoselection cloning method). A positive vector contained a 1.2kb insert. The ability to interfere with the binding of CD27 positive T cells with antigen presenting cells, or the ability to cause such binding to occur on surfaces other than lymphocyte cells, can be useful in diagnostics and therapy. (Updated on 25-MAR-2003 to correct PA field.)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   961 TGGCAGCCACATGCAGTCCCCTTTGTCAGGCCCTTTCCTGTGTACACGTGACA
                                                                            601 GCAGCTGCCCGGACTCTCTCTACCCACTGCCCCCAAAGATCCCTGTGCAGCTC
                                                                                                                                                                                                                                                                CGATTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG
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CAATGGCTGGCAGTGCAGGGACAAGGGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC
                    TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG
                                                                                                                                                     TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG
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                                                            GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCTTACCTTA
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                 /*tag= d
/note= "an additional adenine base at position
given in the specification, but interrupts the
frame"
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Pred. No. 0;
0; Mismatches
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89US-00379076.
90US-00553759.
92US-00983647.
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Best Local Similarity 99.8
Matches 1198; Conservative
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The present sequence is that of cDNA encoding human cell surface antigen (CSA) CD27 (see AAY96137), a T-lymphocyte activation antigen. The CDNA was isolated from a human T-lymphocyte cDNA introduced into COS cells and screened using a novel method of the invention. The method, designed to isolate CSA nucleic acids, is based upon transient expression of a CSA in elevatoric calls and physical selection of cells expression of a CSA in by adhesion to (panning on) an antibody-coated substrate such as a culture dish. CSA nucleic acids isolated by the method of the invention, by adhesion to (panning on) an antibody-coated substrate such as a culture dish. CSA nucleic acids isolated by the method of the invention, and the proteins they encode, are useful for immunocharapeutic applications, diseases, and disorders in animals, inmunocharapeutic applications, diseases, and disorders in animals, including humans. These disorders include asthma, immuno-complex disease, continueding continued asthma, immuno-complex diseases, and incerfere with the binding of CD27 positive T cells with antigen presenting cells, or the ability to ause such binding to occur on presenting cells, can be useful in diagnostics and therapy. A soluble CD27 fusion protein will be useful to prevent the continuedesired T cell proliferation in certain autoimmune diseases
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/*tag= a
/transl except= (pos:200. .202, aa:Arg)
101. .160
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Pred. No. 0;
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Matches 1198; Conservative
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P-PSDB; AAY96137
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13-JUL-1989;
23-MAR-1990;
13-JUL-1990;
01-DEC-1992;
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Screening for agonist or antagonist of Modumet activity, useful for preventing or treating obesity-related diseases, comprises contacting Modumet polypeptide with a test compound and determining extent of polypeptide binding.
                                  type I transmembrane protein, metabolism; body mass; weight loss; obesity; hyperlipidaemia, atherosclerosis; heart disease; stroke; insulin-resistant diabetes; hypertension; cachexia; AIDS-related; cancer-related; weight loss; chronic inflammatory disease-related
                                                                                                                                                                                                                                                                                                                                                           Disclosure, Page 32-33; 38pp; English.
                                                                                                                Location/Qualifiers
101. .883
                                                                                                                                  /*tag= a
/product= "Modumet"
                                                                                                                                                                                                                                                             Ϋ,
                                                                                                                                                                                                                                                            Briggs
                            human; Modumet; tumour
                                                                                                                                                                                                    18-JUL-2002; 2002WO-IB003339
                                                                                                                                                                                                                      20-JUL-2001; 2001US-0306745P
          coding sequence
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                                                                                                                                                               WO2003009862-A1
                                                                          anorexia; ss
                                                                                              Homo sapiens
                                                                                                                                                                                  06-FEB-2003
                                                                                                                                                                                                                                         (GEST )
          Modumet
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This sequence encodes human Modumet. Modumet was used in the method of the invention for screening for an agonist or antagonist of Modumet activity. The method comprises contacting Modumet polypeptide with a test compound, determining the extent of binding of the test compound to the polypeptide, and determining whether the test compounds are agonists or antagonists of the Modumet polypeptide. Modumet is a member of the tumour necrosis factor receptor super family, and is a type I transmembrane protein. The method is useful in metabolic research, particularly, in discovering compounds that modulate Modumet activity or that reduce or increase body mass and maintain weight loss, and in preventing or treating obesity-related diseases or disorders such as hyperlipidaemia, thereosclerosis, heart disease, stroke, insulin-resistant diabetes or hypertension, or for preventing or treating disorders associated with excessive weight loss, such as cachaxia, cancer-related weight loss, AIDS related weight loss, chronic inflammatory disease-related weight loss,

Sequence 1204 BP; 263 A; 376 C; 338 G; 227 T; 0 U; 0 Other;

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                                                      GGGGTGCAAAGAAGAGACAGCAGCCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAAT
            Length 1204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel reagent for diagnosis, molecular definition and therapy of chronic inflammatory joint diseases, and other inflammatory disorders, infective or tumour diseases in humans. The products of the invention have antiinflammatory, cytostatic, antiarthritic, antiinflammatory, cytostatic, and any proteins and unitiodise derived from it, are used (i) for analysing tissue and blood samples for medical diagnosis; (ii) for diagnosis and characterisation of chronic joint diseases, on the basis of molecular characterisation, and determining the etiological pathogemicity principle of as yet creatment of disease, and optimisation of therapy and (iii) for treatments for inflammatory diseases, particularly of joints, infections and tumours. ACA64801-ACA64965 represent human polymucleotides used in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reagents for diagnosis, study and therapy of chronic inflammatory joint and other diseases, comprises any of many specified genes or derived
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                                                                                                                                                                                                                 Human; chronic inflammatory joint disease; infection; tumour;
antiinflammatory; cytostatic; antiarthritic; antirheumatic;
immunosuppressive; gene therapy; etiological pathogenicity; ds.
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03-JUN-2002; 2002US-0385691P.
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protein (e.g. human autotaxin polypeptide), and a further moiety (e.g
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99.6%;
                                                                                                      13-FEB-2003; 2003WO-EP001461
                                                                                                                                        14-FEB-2002; 2002GB-00003480
                                                                                                                                                       29-JUN-2002; 2002GB-00015095
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Matches 1196; Conservative
                                                                                                                                                                                           (BIOI-) BIOINVENT INT AB
                                                                                                                                                                                                                            Borrebaeck CAK,
                                                                                                                                                                                                                                                               WPI; 2003-697496/66.
P-PSDB; ADL15013.
                                  WO2003068268-A2
                                                                     21-AUG-2003
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                                              781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGAGGAGGAGGGCAGCACCAT
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                                                                                                                                                                                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a composition comprising a plurality of cDNAs for detecting the altered expression of genes in an immunological response. The invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comprising obtaining nucleic acids from a sample, contacting the nucleic acids of the sample with an array comprising the plurality of cDNAs under conditions to form one or more hybridisation complexes detected the nucleic conditions to form one or more hybridisation complexes detected in a non-diseased sample, where an altered level of the detected hybridisation complexes or relates with the level of hybridisation complexes or relates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detected complexes and a microarray and a plurality of polynucleotide probes. The cDNAs are useful as hybridisable array elements in a microarray for monitoring the expression of target polynucleotides. The microarray for monitoring the expression of target polynucleotides. The microarray for monitoring the expression of the diseases. The microarray may also be used in drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. The composition of a subpopulation of may also be used in purification of a subpopulation of may also be used in purification of a subpopulation of may also be used in purification of a subpopulation of may also be used in purification of a cut the printing a purality of the discovery and development. Compared to the discovery and development of the discovery and the discovery and the discovery and development of may also be used in purification of a cut the printing part of the discovery and the discovery and the discovery and development of the discovery and the
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                                                                                                                                                                                                                                                                                                                 A composition comprising a plurality of cDNAs, useful for detecting altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCAGAGAGGCACTACTGGGCTCAGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 1027; 50pp; English.
                                                                                                                                                                                                                     Seilhamer JJ;
                                                                       98US-00023655
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Matches 1196; Conservative
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                                                                       09-FEB-1998;
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                    19-AUG-2003
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Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                        soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening;
        tissue sarcoma-upregulated DNA - SEQ ID 2371
                                                                                                                                     (PROT-) PROTEIN DESIGN LABS INC.
                                                                                                   26-NOV-2003; 2003WO-US038193
                                                                                                                    26-NOV-2002; 2002US-0429739P
                                                                                                                                                     Ginsburg WM,
                                                                                                                                                                      WPI; 2004-441208/41
                                                                  WO2004048938-A2
                                                  Homo sapiens
                                                                                   10-JUN-2004
       soft
                                                                                                                                                     Aziz N,
       Human
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Zlotnik A;

sarcoma The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor. Example 2; SEQ ID NO 2371; 210pp; English.

Sequence 1204 BP; 263 A; 376 C; 338 G; 227 T; 0 U; 0 Other;

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                                                                                                                                        CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120
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                                                                                                                                                                                                             GIGGCIGIGCGIICIGGGGACCCIGGIGGGCICICAGCIACICCAGCCCCCAAGAGCIG 180
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Pred. No. 0;
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Query Match
Best Local Similarity 99.6%;
Matches 1196; Conservative
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ss; gene; human; immunological response; blood cell; cancer; immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis;

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bronchitis; ulcerative colitis; diabetes; multiple sclerosis; osteoporosis; pancreatitis; infection; arthritis; lymph node.
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Matches 1196; Conservative
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                                                                                                                                                                                                                                                                                     The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcome the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                          Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                               Example 2; SEQ ID NO 6561; 210pp; English.
                                                                                                                                        Zlotnik A;
                                                                                                           (PROT-) PROTEIN DESIGN LABS INC
                                                      26-NOV-2003; 2003WO-US038193
                                                                                26-NOV-2002; 2002US-0429739P
                                                                                                                                       Ginsburg WM,
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98.5%; Score 1182.6; DB 12; Length 1711;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1196; Conservative 0; Mismatches 4; Indels 1; C
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Sequence 1711 BP; 441 A; 524 C; 472 G; 274 T; 0 U; 0 Other;